SEQUENCE LISTING

<110> AKZO Nobel N.V.

<120> novel *Brachyspira hyodysenteriae* vaccine

<130> Bhyovaccine

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 1614

<212> DNA

<213> Brachyspira hyodysenteria

<220>

<221> CDS

<222> (1)..(1611)

<223>

<400> 1

```
atg aaa aaa cta tat tca tta ttt ata ttt ata gct gta att tta ttt       48
Met Lys Lys Leu Tyr Ser Leu Phe Ile Phe Ile Ala Val Ile Leu Phe
1               5                  10                  15

att tat tca tgc gga agt tat ttt aat cct aaa tac tat ttt ttt aaa       96
Ile Tyr Ser Cys Gly Ser Tyr Phe Asn Pro Lys Tyr Tyr Phe Phe Lys
            20                  25                  30

agt aaa gta gag aat aat gga agt tct gga agc tca ggc ggt aat tca      144
Ser Lys Val Glu Asn Asn Gly Ser Ser Gly Ser Ser Gly Gly Asn Ser
        35                  40                  45
```

```
gga ata tat ata cag cct ggt gaa gat gaa gat cct ttt aca gca cct      192
Gly Ile Tyr Ile Gln Pro Gly Glu Asp Glu Asp Pro Phe Thr Ala Pro
    50                  55                  60

aaa tat gca tct gag tgg tgg aat gat cct aat aat ggt gga ttt gat      240
Lys Tyr Ala Ser Glu Trp Trp Asn Asp Pro Asn Asn Gly Gly Phe Asp
65                  70                  75                  80

gct tcg gat ata gat aaa tgg ttt ttg aaa gtt gaa ttt tta gca aat      288
Ala Ser Asp Ile Asp Lys Trp Phe Leu Lys Val Glu Phe Leu Ala Asn
                85                  90                  95

gat tat cca agt tac aga ttt tta aca aaa agc gga aga aaa gca gga      336
Asp Tyr Pro Ser Tyr Arg Phe Leu Thr Lys Ser Gly Arg Lys Ala Gly
            100                 105                 110

cat gtt tgg gta gtt tct aat gaa caa tct cag gca tat tta gat caa      384
His Val Trp Val Val Ser Asn Glu Gln Ser Gln Ala Tyr Leu Asp Gln
        115                 120                 125

gga gaa gta tgc aat act aca gca gtt acc ggg gta tct ata aaa cca      432
Gly Glu Val Cys Asn Thr Thr Ala Val Thr Gly Val Ser Ile Lys Pro
    130                 135                 140

gta gca aat gta aca gga gta aca tat aca aaa tat aag gga ttg aat      480
Val Ala Asn Val Thr Gly Val Thr Tyr Thr Lys Tyr Lys Gly Leu Asn
145                 150                 155                 160

gca aga ttt ttc act cat gac gga gat tat cat aat gta tat cct gga      528
Ala Arg Phe Phe Thr His Asp Gly Asp Tyr His Asn Val Tyr Pro Gly
                165                 170                 175

aaa gat aag ata agc aga ttc tat ttt tat tat ttt aca ggt act ccg      576
Lys Asp Lys Ile Ser Arg Phe Tyr Phe Tyr Tyr Phe Thr Gly Thr Pro
            180                 185                 190

gaa atg gct aaa ttt tta gaa aat tgc tta ata gct gta gac aca tac      624
Glu Met Ala Lys Phe Leu Glu Asn Cys Leu Ile Ala Val Asp Thr Tyr
        195                 200                 205

tca aaa cta tta ttt tac tat gga aga cct caa agc gat tat cca aat      672
Ser Lys Leu Leu Phe Tyr Tyr Gly Arg Pro Gln Ser Asp Tyr Pro Asn
    210                 215                 220

cct cca agc tgg cag aag cct agt aat ttg gtt gat aaa tac tct cct      720
Pro Pro Ser Trp Gln Lys Pro Ser Asn Leu Val Asp Lys Tyr Ser Pro
225                 230                 235                 240

aca ggt tat tgg ata tct ata gat gaa ggt ata aat gat aag ggg cag      768
Thr Gly Tyr Trp Ile Ser Ile Asp Glu Gly Ile Asn Asp Lys Gly Gln
                245                 250                 255

aat tat cct ttt tat gaa tat gat cct gta gga tat gta aaa agc gat      816
Asn Tyr Pro Phe Tyr Glu Tyr Asp Pro Val Gly Tyr Val Lys Ser Asp
            260                 265                 270

ggt aca gtt gtt ata ttt gat tgg ttt gca aac aga tta aga gga aat      864
```

```
Gly Thr Val Val Ile Phe Asp Trp Phe Ala Asn Arg Leu Arg Gly Asn
        275                 280                 285

cat aat aat gat cct ata aaa agt gat cct aaa gga gct att gtt cct      912
His Asn Asn Asp Pro Ile Lys Ser Asp Pro Lys Gly Ala Ile Val Pro
    290                 295                 300

aat cct aat act aat cct tct gct tca act aca gga cgt tct cct tat      960
Asn Pro Asn Thr Asn Pro Ser Ala Ser Thr Thr Gly Arg Ser Pro Tyr
305                 310                 315                 320

gca ttc tat tcg cct tta gca caa aaa gat aaa act aaa ata act ata     1008
Ala Phe Tyr Ser Pro Leu Ala Gln Lys Asp Lys Thr Lys Ile Thr Ile
                325                 330                 335

agt act aca aaa tta ata aat tat aca gtt ttc agt tat aaa tac agt     1056
Ser Thr Thr Lys Leu Ile Asn Tyr Thr Val Phe Ser Tyr Lys Tyr Ser
            340                 345                 350

ata caa ata ttt ccg cct agt atg aaa gaa gaa aaa ctt cct tat gct     1104
Ile Gln Ile Phe Pro Pro Ser Met Lys Glu Glu Lys Leu Pro Tyr Ala
        355                 360                 365

tat att gca tat gct tcc tat ggt gca gct tat caa aat gaa agc agc     1152
Tyr Ile Ala Tyr Ala Ser Tyr Gly Ala Ala Tyr Gln Asn Glu Ser Ser
    370                 375                 380

aaa tct gta gag atg ata tct gat ata aat aaa gga gag cat tac gga     1200
Lys Ser Val Glu Met Ile Ser Asp Ile Asn Lys Gly Glu His Tyr Gly
385                 390                 395                 400

agt att aca aga ata agc act gta cct aaa ata gat aaa gac gga gga     1248
Ser Ile Thr Arg Ile Ser Thr Val Pro Lys Ile Asp Lys Asp Gly Gly
                405                 410                 415

gag ttg gta aaa gaa gga tct aag tct ttt gaa tta tat ggt att gat     1296
Glu Leu Val Lys Glu Gly Ser Lys Ser Phe Glu Leu Tyr Gly Ile Asp
            420                 425                 430

act aaa gat aca ttt ata gaa tta agt tta aaa cta att aaa aat gat     1344
Thr Lys Asp Thr Phe Ile Glu Leu Ser Leu Lys Leu Ile Lys Asn Asp
        435                 440                 445

gaa aat aca gaa ttt gtt gat caa gga aca gca ggt act ggt cct tta     1392
Glu Asn Thr Glu Phe Val Asp Gln Gly Thr Ala Gly Thr Gly Pro Leu
    450                 455                 460

gta tac ttt gat aaa aca gat cct ata ctt gta tta aaa tat gat aaa     1440
Val Tyr Phe Asp Lys Thr Asp Pro Ile Leu Val Leu Lys Tyr Asp Lys
465                 470                 475                 480

tct tct gac agc ttc aaa tac agc agt gta aaa gga aac aag caa ata     1488
Ser Ser Asp Ser Phe Lys Tyr Ser Ser Val Lys Gly Asn Lys Gln Ile
                485                 490                 495

gaa gtt gac agc aat tta tca att aaa aga gga gag aat aaa gag ttt     1536
Glu Val Asp Ser Asn Leu Ser Ile Lys Arg Gly Glu Asn Lys Glu Phe
```

```
            500                 505                 510

aca gtt aaa ttt aaa gat cca aat aat gga aat gag ttt ggg gtt gta      1584
Thr Val Lys Phe Lys Asp Pro Asn Asn Gly Asn Glu Phe Gly Val Val
        515                 520                 525

ttt aaa ata gat ttt gaa aaa ata tca tga                            1614
Phe Lys Ile Asp Phe Glu Lys Ile Ser
    530                 535
```

<210> 2

<211> 537

<212> PRT

<213> Brachyspira hyodysenteria

<400> 2

```
Met Lys Lys Leu Tyr Ser Leu Phe Ile Phe Ile Ala Val Ile Leu Phe
1               5                   10                  15

Ile Tyr Ser Cys Gly Ser Tyr Phe Asn Pro Lys Tyr Tyr Phe Phe Lys
            20                  25                  30

Ser Lys Val Glu Asn Asn Gly Ser Ser Gly Ser Ser Gly Gly Asn Ser
        35                  40                  45

Gly Ile Tyr Ile Gln Pro Gly Glu Asp Glu Asp Pro Phe Thr Ala Pro
    50                  55                  60

Lys Tyr Ala Ser Glu Trp Trp Asn Asp Pro Asn Asn Gly Gly Phe Asp
65                  70                  75                  80

Ala Ser Asp Ile Asp Lys Trp Phe Leu Lys Val Glu Phe Leu Ala Asn
                85                  90                  95

Asp Tyr Pro Ser Tyr Arg Phe Leu Thr Lys Ser Gly Arg Lys Ala Gly
            100                 105                 110

His Val Trp Val Val Ser Asn Glu Gln Ser Gln Ala Tyr Leu Asp Gln
        115                 120                 125

Gly Glu Val Cys Asn Thr Thr Ala Val Thr Gly Val Ser Ile Lys Pro
    130                 135                 140
```

```
Val Ala Asn Val Thr Gly Val Thr Tyr Thr Lys Tyr Lys Gly Leu Asn
145                 150                 155                 160

Ala Arg Phe Phe Thr His Asp Gly Asp Tyr His Asn Val Tyr Pro Gly
                165                 170                 175

Lys Asp Lys Ile Ser Arg Phe Tyr Phe Tyr Tyr Phe Thr Gly Thr Pro
            180                 185                 190

Glu Met Ala Lys Phe Leu Glu Asn Cys Leu Ile Ala Val Asp Thr Tyr
        195                 200                 205

Ser Lys Leu Leu Phe Tyr Tyr Gly Arg Pro Gln Ser Asp Tyr Pro Asn
    210                 215                 220

Pro Pro Ser Trp Gln Lys Pro Ser Asn Leu Val Asp Lys Tyr Ser Pro
225                 230                 235                 240

Thr Gly Tyr Trp Ile Ser Ile Asp Glu Gly Ile Asn Asp Lys Gly Gln
                245                 250                 255

Asn Tyr Pro Phe Tyr Glu Tyr Asp Pro Val Gly Tyr Val Lys Ser Asp
            260                 265                 270

Gly Thr Val Val Ile Phe Asp Trp Phe Ala Asn Arg Leu Arg Gly Asn
        275                 280                 285

His Asn Asn Asp Pro Ile Lys Ser Asp Pro Lys Gly Ala Ile Val Pro
    290                 295                 300

Asn Pro Asn Thr Asn Pro Ser Ala Ser Thr Thr Gly Arg Ser Pro Tyr
305                 310                 315                 320

Ala Phe Tyr Ser Pro Leu Ala Gln Lys Asp Lys Thr Lys Ile Thr Ile
                325                 330                 335

Ser Thr Thr Lys Leu Ile Asn Tyr Thr Val Phe Ser Tyr Lys Tyr Ser
            340                 345                 350

Ile Gln Ile Phe Pro Pro Ser Met Lys Glu Glu Lys Leu Pro Tyr Ala
        355                 360                 365
```

```
Tyr Ile Ala Tyr Ala Ser Tyr Gly Ala Ala Tyr Gln Asn Glu Ser Ser
    370                 375                 380

Lys Ser Val Glu Met Ile Ser Asp Ile Asn Lys Gly Glu His Tyr Gly
385                 390                 395                 400

Ser Ile Thr Arg Ile Ser Thr Val Pro Lys Ile Asp Lys Asp Gly Gly
                405                 410                 415

Glu Leu Val Lys Glu Gly Ser Lys Ser Phe Glu Leu Tyr Gly Ile Asp
            420                 425                 430

Thr Lys Asp Thr Phe Ile Glu Leu Ser Leu Lys Leu Ile Lys Asn Asp
        435                 440                 445

Glu Asn Thr Glu Phe Val Asp Gln Gly Thr Ala Gly Thr Gly Pro Leu
    450                 455                 460

Val Tyr Phe Asp Lys Thr Asp Pro Ile Leu Val Leu Lys Tyr Asp Lys
465                 470                 475                 480

Ser Ser Asp Ser Phe Lys Tyr Ser Ser Val Lys Gly Asn Lys Gln Ile
                485                 490                 495

Glu Val Asp Ser Asn Leu Ser Ile Lys Arg Gly Glu Asn Lys Glu Phe
            500                 505                 510

Thr Val Lys Phe Lys Asp Pro Asn Asn Gly Asn Glu Phe Gly Val Val
        515                 520                 525

Phe Lys Ile Asp Phe Glu Lys Ile Ser
    530                 535
```

<210> 3

<211> 540

<212> DNA

<213> Brachyspira hyodysenteria

<220>

<221> CDS

<222> (1)..(537)

<223>

<400> 3

```
atg ttt aag aaa ctt ttt att gtt gtg ggt ttg atg agt gtg ctt gct       48
Met Phe Lys Lys Leu Phe Ile Val Val Gly Leu Met Ser Val Leu Ala
1               5                  10                  15

gga tgt gaa act atg cag cct aaa aat aat gat aca att gta aaa aat       96
Gly Cys Glu Thr Met Gln Pro Lys Asn Asn Asp Thr Ile Val Lys Asn
            20                  25                  30

gat aat tca tct aat gaa gat aaa aaa gaa gaa act ata act aga gaa      144
Asp Asn Ser Ser Asn Glu Asp Lys Lys Glu Glu Thr Ile Thr Arg Glu
        35                  40                  45

gat aca cca aaa atg aaa gtt aca gtt tat gga gca gat aaa gaa att      192
Asp Thr Pro Lys Met Lys Val Thr Val Tyr Gly Ala Asp Lys Glu Ile
    50                  55                  60

caa gct gtg gaa ata aat gat aaa act tat tat gta ata ggc gga aaa      240
Gln Ala Val Glu Ile Asn Asp Lys Thr Tyr Tyr Val Ile Gly Gly Lys
65                  70                  75                  80

gat gtt gag aat atg aca gaa gct gat ata aaa aaa tca tct tta gta      288
Asp Val Glu Asn Met Thr Glu Ala Asp Ile Lys Lys Ser Ser Leu Val
                85                  90                  95

gca cct tta aaa gtt aca gaa gaa act gtt aat ggt aca aga ggt ata      336
Ala Pro Leu Lys Val Thr Glu Glu Thr Val Asn Gly Thr Arg Gly Ile
            100                 105                 110

gtt gtt aca tat tat gat gta aaa gta ttc ttg ggt aaa aga aca gga      384
Val Val Thr Tyr Tyr Asp Val Lys Val Phe Leu Gly Lys Arg Thr Gly
        115                 120                 125

aca gga act atc gta gga ata ttc gag cct cag aaa aat gat tgg act      432
Thr Gly Thr Ile Val Gly Ile Phe Glu Pro Gln Lys Asn Asp Trp Thr
    130                 135                 140

aca gga aat gat ttg gat aga agt tta tct att caa ata aaa tta tct      480
Thr Gly Asn Asp Leu Asp Arg Ser Leu Ser Ile Gln Ile Lys Leu Ser
145                 150                 155                 160

aga aat ata gca ggt cct ata gat ata aaa aga gga agc ata tct tta      528
Arg Asn Ile Ala Gly Pro Ile Asp Ile Lys Arg Gly Ser Ile Ser Leu
                165                 170                 175

gca ttt aat taa                                                     540
Ala Phe Asn
```

<210> 4

<211> 179

<212> PRT

<213> Brachyspira hyodysenteria

<400> 4

Met Phe Lys Lys Leu Phe Ile Val Val Gly Leu Met Ser Val Leu Ala
1 5 10 15

Gly Cys Glu Thr Met Gln Pro Lys Asn Asn Asp Thr Ile Val Lys Asn
20 25 30

Asp Asn Ser Ser Asn Glu Asp Lys Lys Glu Glu Thr Ile Thr Arg Glu
35 40 45

Asp Thr Pro Lys Met Lys Val Thr Val Tyr Gly Ala Asp Lys Glu Ile
50 55 60

Gln Ala Val Glu Ile Asn Asp Lys Thr Tyr Tyr Val Ile Gly Gly Lys
65 70 75 80

Asp Val Glu Asn Met Thr Glu Ala Asp Ile Lys Lys Ser Ser Leu Val
85 90 95

Ala Pro Leu Lys Val Thr Glu Glu Thr Val Asn Gly Thr Arg Gly Ile
100 105 110

Val Val Thr Tyr Tyr Asp Val Lys Val Phe Leu Gly Lys Arg Thr Gly
115 120 125

Thr Gly Thr Ile Val Gly Ile Phe Glu Pro Gln Lys Asn Asp Trp Thr
130 135 140

Thr Gly Asn Asp Leu Asp Arg Ser Leu Ser Ile Gln Ile Lys Leu Ser
145 150 155 160

Arg Asn Ile Ala Gly Pro Ile Asp Ile Lys Arg Gly Ser Ile Ser Leu
165 170 175

Ala Phe Asn